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1023#8 OIPE
by
15-02

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/859,604

DATE: 10/11/2001

TIME: 09:21:13

Input Set : A:\Rih32cil.app

Output Set: N:\CRF3\10112001\I859604.raw

3 <110> APPLICANT: Wands, Jack R.
 4 de la Monte, Suzanne M
 5 Deutch, Alan H
 6 Ghanbari, Hossein A
 8 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
 10 <130> FILE REFERENCE: 21486-032 CIP
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/859,604
 13 <141> CURRENT FILING DATE: 2001-05-17
 15 <150> PRIOR APPLICATION NUMBER: 09/436,184
 16 <151> PRIOR FILING DATE: 1999-11-08
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 36
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
 29 EGF-like domain
 31 <220> FEATURE:
 32 <221> NAME/KEY: VARIANT
 33 <222> LOCATION: (2)..(8)
 34 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid
 36 <220> FEATURE:
 37 <221> NAME/KEY: VARIANT
 38 <222> LOCATION: (10)..(13)
 39 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 41 <220> FEATURE:
 42 <221> NAME/KEY: VARIANT
 43 <222> LOCATION: (15)..(24)
 44 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 46 <220> FEATURE:
 47 <221> NAME/KEY: VARIANT
 48 <222> LOCATION: (26)
 49 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 51 <220> FEATURE:
 52 <221> NAME/KEY: VARIANT
 53 <222> LOCATION: (28)..(35)
 54 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 56 <400> SEQUENCE: 1
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 58 1 5 10 15
 W--> 60 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa
 61 20 25 30
 W--> 63 Xaa Xaa Xaa Cys
 64 35
 67 <210> SEQ ID NO: 2

ENTERED

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68 <211> LENGTH: 758
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 2
73 Met Ala Gln Arg Lys Asn Ala Lys Ser Ser Gly Asn Ser Ser Ser Ser
74   1           5           10           15
76 Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
77           20           25           30
79 Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
80           35           40           45
82 Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
83           50           55           60
85 Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
86   65           70           75           80
88 Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
89           85           90           95
91 Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
92           100          105          110
94 Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
95           115          120          125
97 Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
98           130          135          140
100 Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
101 145          150          155          160
103 Ala Glu His Val Glu Gly Glu Asp Leu Gln Glu Asp Gly Pro Thr
104           165          170          175
106 Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
107           180          185          190
109 Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
110           195          200          205
112 Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
113           210          215          220
115 Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
116 225          230          235          240
118 Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
119           245          250          255
121 Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
122           260          265          270
124 Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
125           275          280          285
127 Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
128           290          295          300
130 Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
131 305          310          315          320
133 Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys
134           325          330          335
136 Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
137           340          345          350
139 Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val

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140          355          360          365
142 Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys
143          370          375          380
145 Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly
146 385          390          395          400
148 Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala
149          405          410          415
151 Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe
152          420          425          430
154 Leu Gly His Met Arg Gly Ser Leu Thr Leu Gln Arg Leu Val Gln
155          435          440          445
157 Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr
158          450          455          460
160 Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Glu Val
161 465          470          475          480
163 Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe
164          485          490          495
166 Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys
167          500          505          510
169 Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr
170          515          520          525
172 Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr
173          530          535          540
175 Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp
176 545          550          555          560
178 Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp
179          565          570          575
181 Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg
182          580          585          590
184 Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala
185          595          600          605
187 Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp
188          610          615          620
190 Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala
191 625          630          635          640
193 Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu
194          645          650          655
196 Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro
197          660          665          670
199 Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg
200          675          680          685
202 Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys
203          690          695          700
205 Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp
206 705          710          715          720
208 Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu
209          725          730          735
211 Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg
212          740          745          750

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214 Arg Ser Leu Pro Ala Ile

215 755

218 <210> SEQ ID NO: 3

219 <211> LENGTH: 2324

220 <212> TYPE: DNA

221 <213> ORGANISM: Homo sapiens

223 <400> SEQUENCE: 3

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224 cggaccgtgc aatggcccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 60
225 gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccgg agagagacaa 120
226 agcatggagg acacaagaat gggaggaaag gcggactctc gggaacttca ttcttcacgt 180
227 ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcggt tggtttgatc 240
228 ttgttgacta tgaggaaagt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 300
229 attttgatgt ggtgatgcc aaagttttat taggacttaa agagagatct acttcagagc 360
230 cagcagtcgc gccagaagag gctgagccac aactgagcc cgaggagcag gttcctgtgg 420
231 aggcagaacc ccagaatatc gaagatgaag caaaagaaca aattcagtc cttctccatg 480
232 aaatggtaca cgcagaacat gttgaggagg aagacttgca acaagaagat ggaccacag 540
233 gagaaccaca acaagaggat gatgagtttc ttatggcgac tgatgtagat gatagatttg 600
234 agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 660
235 cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 720
236 attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 780
237 accaagtcta tgaggaaaca gcagtatatg aacctctaga aatgaaggg atagaaatca 840
238 cagaagtaac tgctccccct gaggataatc ctgtagaaga ttcacaggta attgtagaag 900
239 aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 960
240 cagatgatcc agaacaaaaa gcaaaagtta agaaaaagaa gcctaaactt ttaaataaat 1020
241 ttgataagac tattaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1080
242 ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1140
243 caagatatgg gaaggcgagc tgtgaggatg atttggctga gaagaggaga agtaattgag 1200
244 tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgagc 1260
245 acctgctgaa gctgagtttg aagcgtcgct cagacaggca acaatttcta ggtcatatga 1320
246 gaggttcctt gcttaccctg cagagattag ttcaactatt tcccaatgat acttccttaa 1380
247 aaaatgacct tggcgtggga tacctcttga taggagataa tgacaatgca aagaaagttt 1440
248 atgaagaggt gctgagtgtg acacctaatg atggctttgc taaagtccat tatggcttca 1500
249 tcctgaaggc acagaacaaa attgctgaga gcattccata tttaaaggaa ggaatagaat 1560
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254 tccgagatga aggccttgca gtgatggata aagccaaagg tctcttcctg cctgaggatg 1860
255 aaaacctgag ggaaaaaggg gactggagcc agttcacgct gtggcagcaa ggaagaagaa 1920
256 atgaaaatgc ctgcaaagga gctcctaaaa cctgtacctt actagaaaag ttccccgaga 1980
257 caacaggatg cagaagagga cagatcaaat attccatcat gcaccccggt actcacgtgt 2040
258 ggccgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2100
259 aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaaggtgc 2160
260 tcactcttga tgactccttt gagcacgagg tatggcagga tgccctcatc ttccggctga 2220
261 tattcatcgt ggaatgtgtg catccggaac tgacaccaca gcagagacgc agccttcagc 2280
262 caatttagca tgaattcatg caagcttggg aaactctgga gaga 2324
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 31
267 <212> TYPE: PRT

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268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: EGF-like
272     cysteine-rich repeat
274 <220> FEATURE:
275 <221> NAME/KEY: VARIANT
276 <222> LOCATION: (2)..(5)
277 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid
279 <220> FEATURE:
280 <221> NAME/KEY: VARIANT
281 <222> LOCATION: (7)..(8)
282 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
284 <220> FEATURE:
285 <221> NAME/KEY: VARIANT
286 <222> LOCATION: (10)
287 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
289 <220> FEATURE:
290 <221> NAME/KEY: VARIANT
291 <222> LOCATION: (14)
292 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
294 <220> FEATURE:
295 <221> NAME/KEY: VARIANT
296 <222> LOCATION: (17)..(18)
297 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
299 <220> FEATURE:
300 <221> NAME/KEY: VARIANT
301 <222> LOCATION: (25)..(26)
302 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
304 <220> FEATURE:
305 <221> NAME/KEY: VARIANT
306 <222> LOCATION: (29)
307 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
309 <400> SEQUENCE: 4
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311     1         5         10        15
W--> 313 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys
314         20         25         30
317 <210> SEQ ID NO: 5
318 <211> LENGTH: 1242
319 <212> TYPE: PRT
320 <213> ORGANISM: Homo sapiens
322 <400> SEQUENCE: 5
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324     1         5         10        15
326 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
327         20         25         30
329 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
330         35         40         45
332 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile

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VERIFICATION SUMMARY

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Input Set : A:\Rih32cil.app

Output Set: N:\CRF3\10112001\I859604.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4